

RAW SEQUENCE LISTING DATE: 01/07/2002 PATENT APPLICATION: US/09/378,261 TIME: 14:39:31

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Output Set: N:\CRF3\01072002\I378261.raw

## #9

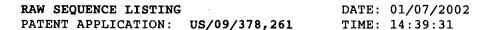
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SEQUENCE LISTING
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3 (1) GENERAL INFORMATION:
      5
             (i) APPLICANT: Fukudome, Kenji
      6
                            Esmon, Charles T.
      8
            (ii) TITLE OF INVENTION: Cloning and Regulation of an Endothelial
     9
                                     Cell Protein C/Activated Protein C Receptor
     11
           (iii) NUMBER OF SEQUENCES: 6
     13
            (iv) CORRESPONDENCE ADDRESS:
     14
                  (A) ADDRESSEE: Patrea L. Pabst
                  (B) STREET: 2800 One Atlantic Center, 1201 West Peachtree
     15
                              Street
     16
     17
                  (C) CITY: Atlanta
                  (D) STATE: Georgia
     18
                                                       ENTEREL
     19
                  (E) COUNTRY: US
                  (F) ZIP: 30306-3450
     20
             (V) COMPUTER READABLE FORM:
     22
                  (A) MEDIUM TYPE: Floppy disk
     23
     24
                  (B) COMPUTER: IBM PC compatible
                  (C) OPERATING SYSTEM: PC-DOS/MS-DOS
     25
     26
                  (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
     28
            (vi) CURRENT APPLICATION DATA:
                  (A) APPLICATION NUMBER: US/09/378,261
C--> 29
C--> 30
                  (B) FILING DATE: 20-Aug-1999
     31
                  (C) CLASSIFICATION:
           (vii) PRIOR APPLICATION DATA:
     33
     34
                  (A) APPLICATION NUMBER: 08/289,699
     35
                  (B) FILING DATE: 12-AUG-1994
          (viii) ATTORNEY/AGENT INFORMATION:
     38
     39
                  (A) NAME: Pabst, Patrea L.
                  (B) REGISTRATION NUMBER: 31,284
     40
     41
                  (C) REFERENCE/DOCKET NUMBER: OMRF152
     43
            (ix) TELECOMMUNICATION INFORMATION:
     44
                  (A) TELEPHONE: (404)873-8794
     45
                  (B) TELEFAX: (404)873-8795
     48 (2) INFORMATION FOR SEQ ID NO: 1:
     50
             (i) SEQUENCE CHARACTERISTICS:
     51
                  (A) LENGTH: 1302 base pairs
     52
                  (B) TYPE: nucleic acid
                  (C) STRANDEDNESS: single
     53
     54
                  (D) TOPOLOGY: linear
     56
            (ii) MOLECULE TYPE: cDNA
     58
           (iii) HYPOTHETICAL: NO
     60
            (iv) ANTI-SENSE: NO
     62
            (ix) FEATURE:
     63
                  (A) NAME/KEY: misc_feature
     64
                  (B) LOCATION: 1..1302
     65
                  (D) OTHER INFORMATION: /note= "Nucleotides 25 through 738 encode the
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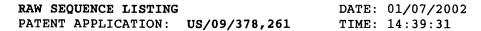
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Output Set: N:\CRF3\01072002\I378261.raw

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67 Endothelial Cell Protein Receptor of Sequence ID No. 2."
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
71 CAGGTCCGGA GCCTCAACTT CAGGATGTTG ACAACATTGC TGCCGATACT GCTGCTGTCT
                                                                          60
73 GGCTGGGCCT TTTGTAGCCA AGACGCCTCA GATGGCCTCC AAAGACTTCA TATGCTCCAG
                                                                         120
75 ATCTCCTACT TCCGCGACCC CTATCACGTG TGGTACCAGG GCAACGCGTC GCTGGGGGGA
                                                                         180
77 CACCTAACGC ACGTGCTGGA AGGCCCAGAC ACCAACACCA CGATCATTCA GCTGCAGCCC
                                                                         240
79 TTGCAGGAGC CCGAGAGCTG GGCGCGCACG CAGAGTGGCC TGCAGTCCTA CCTGCTCCAG
                                                                         300
81 TTCCACGGCC TCGTGCGCCT GGTGCACCAG GAGCGGACCT TGGCCTTTCC TCTGACCATC
                                                                         360
83 CGCTGCTTCC TGGGCTGTGA GCTGCCTCCC GAGGGCTCTA GAGCCCATGT CTTCTTCGAA
                                                                         420
85 GTGGCTGTGA ATGGGAGCTC CTTTGTGAGT TTCCGGCCGG AGAGAGCCTT GTGGCAGGCA
                                                                         480
87 GACACCCAGG TCACCTCCGG AGTGGTCACC TTCACCCTGC AGCAGCTCAA TGCCTACAAC
                                                                         540
89 CGCACTCGGT ATGAACTGCG GGAATTCCTG GAGGACACCT GTGTGCAGTA TGTGCAGAAA
                                                                         600
91 CATATTTCCG CGGAAAACAC GAAAGGGAGC CAAACAAGCC GCTCCTACAC TTCGCTGGTC
                                                                         660
93 CTGGGCGTCC TGGTGGGCGG TTTCATCATT GCTGGTGTGG CTGTAGGCAT CTTCCTGTGC
                                                                         720
95 ACAGGTGGAC GGCGATGTTA ATTACTCTCC AGCCCCGTCA GAAGGGGCTG GATTGATGGA
                                                                         780
97 GGCTGGCAAG GGAAAGTTTC AGCTCACTGT GAAGCCAGAC TCCCCAACTG AAACACCAGA
                                                                         840
99 AGGTTTGGAG TGACAGCTCC TTTCTTCTCC CACATCTGCC CACTGAAGAT TTGAGGGAGG
                                                                         900
101 GGAGATGGAG AGGAGAGGTG GACAAAGTAC TTGGTTTGCT AAGAACCTAA GAACGTGTAT
                                                                          960
103 GCTTTGCTGA ATTAGTCTGA TAAGTGAATG TTTATCTATC TTTGTGGAAA ACAGATAATG
                                                                         1020
105 GAGTTGGGGC AGGAAGCCTA TGCGCCATCC TCCAAAGACA GACAGAATCA CCTGAGGCGT
                                                                         1080
107 TCAAAAGATA TAACCAAATA AACAAGTCAT CCACAATCAA AATACAACAT TCAATACTTC
                                                                         1140
109 CAGGTGTGTC AGACTTGGGA TGGGACGCTG ATATAATAGG GTAGAAAGAA GTAACACGAA
                                                                         1200
111 GAAGTGGTGG AAATGTAAAA TCCAAGTCAT ATGGCAGTGA TCAATTATTA ATCAATTAAT
                                                                         1260
1302
115 (2) INFORMATION FOR SEQ ID NO: 2:
116
         (i) SEQUENCE CHARACTERISTICS:
117
              (A) LENGTH: 238 amino acids
118
              (B) TYPE: amino acid
119
              (D) TOPOLOGY: linear
121
        (ii) MOLECULE TYPE: protein
123
       (iii) HYPOTHETICAL: NO
        (ix) FEATURE:
125
126
              (A) NAME/KEY: misc_feature
127
              (B) LOCATION: 1..365
128
              (D) OTHER INFORMATION: /note= "Endothelial Cell Protein Receptor
129 encoded by
130 nucleotides 1 through 1302 of Sequence ID No. 1."
131
        (ix) FEATURE:
132
              (A) NAME/KEY: Modified-site
133
              (B) LOCATION: 1..15
134
              (D) OTHER INFORMATION: /note= "Amino acids 1-15 represent
135 a putative signal sequence."
137
        (ix) FEATURE:
138
              (A) NAME/KEY: Domain
              (B) LOCATION: 211..236
139
              (D) OTHER INFORMATION: /note= "Amino acids 211-236
140
141 represent a putative transmembrane domain."
143
        (ix) FEATURE:
144
              (A) NAME/KEY: Active-site
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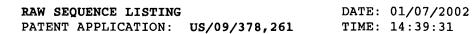
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(B) LOCATION: 47..174
145
              (D) OTHER INFORMATION: /note= "Amino acids 47-49, 64-66,
146
147 136-138 and 172-174 represent potential
148 N-glycosylation sites."
        (ix) FEATURE:
150
151
              (A) NAME/KEY: Modified-site
152
              (B) LOCATION: 17..186
              (D) OTHER INFORMATION: /note= "Amino acids 17, 114, 118
153
154 and 186 represent extracellular cysteine
155 residues."
157
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
159
         Met Leu Thr Thr Leu Leu Pro Ile Leu Leu Ser Gly Trp Ala Phe
160
162
         Cys Ser Gln Asp Ala Ser Asp Gly Leu Gln Arg Leu His Met Leu Gln
163
                                          25
165
         Ile Ser Tyr Phe Arg Asp Pro Tyr His Val Trp Tyr Gln Gly Asn Ala
166
                                      40
168
         Ser Leu Gly Gly His Leu Thr His Val Leu Glu Gly Pro Asp Thr Asn
169
                                 55
171
         Thr Thr Ile Ile Gln Leu Gln Pro Leu Gln Glu Pro Glu Ser Trp Ala
172
                             70
                                                  75
174
         Arg Thr Gln Ser Gly Leu Gln Ser Tyr Leu Leu Gln Phe His Gly Leu
175
177
         Val Arg Leu Val His Gln Glu Arg Thr Leu Ala Phe Pro Leu Thr Ile
178
                     100
                                          105
180
         Arg Cys Phe Leu Gly Cys Glu Leu Pro Pro Glu Gly Ser Arg Ala His
181
                                      120
183
         Val Phe Phe Glu Val Ala Val Asn Gly Ser Ser Phe Val Ser Phe Arg
184
                                 135
186
         Pro Glu Arg Ala Leu Trp Gln Ala Asp Thr Gln Val Thr Ser Gly Val
187
                             150
                                                  155
189
         Val Thr Phe Thr Leu Gln Gln Leu Asn Ala Tyr Asn Arg Thr Arg Tyr
190
                         165
                                              170
193
         Glu Leu Arg Glu Phe Leu Glu Asp Thr Cys Val Gln Tyr Val Gln Lys
194
                                          185
196
         His Ile Ser Ala Glu Asn Thr Lys Gly Ser Gln Thr Ser Arg Ser Tyr
197
                                      200
200
         Thr Ser Leu Val Leu Gly Val Leu Val Gly Phe Ile Ile Ala Gly
201
                                 215
                                                      220
203
         Val Ala Val Gly Ile Phe Leu Cys Thr Gly Gly Arg Arg Cys
                                                  235
206 (2) INFORMATION FOR SEQ ID NO: 3:
         (i) SEQUENCE CHARACTERISTICS:
208
209
              (A) LENGTH: 244 amino acids
210
              (B) TYPE: amino acid
211
              (C) STRANDEDNESS: single
212
              (D) TOPOLOGY: linear
        (ii) MOLECULE TYPE: peptide
214
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
216
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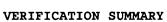
Input Set : N:\Crf3\RULE60\09378261.raw
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218		_	Leu	Thr	Lys	Phe	Leu	Leu	Leu	Leu		Leu	Leu	Leu	Pro		Cys
219		1	Dha	17n 1	mh m	5	No.	31.	D	T	10	31 <u>-</u>	·	31-	D	15	T
221 222		АІА	Pile	Val	Thr 20	PIO	met	Ата	PIO	шуs 25	Ата	Ald	TYL	Ата	30	ASP	Leu
224		T.Au	Dho	Pro	Arg	Dro	Dro	Sor	Cve		λla	Sar	Glv	Gln		Sar	T.Ou
225		LCu	1110	35	9	110	110	UCI	40	Olu	niu	DCI	OLY	45	nry	DCI	пец
227		Glv	Lvs		Leu	Thr	His	Thr		Glu	Glv	Pro	Ser		Asn	Val	Thr
228		1	50					55					60	0111		, 44	
230		Ile		Gln	Leu	Gln	Pro		Gln	Asp	Pro	Glu		Trp	Glu	Ara	Thr
231		65					70					75				3	80
233		Glu	Ser	Gly	Leu	Gln	Ile	Tyr	Leu	Thr	Gln	Phe	Glu	Ser	Leu	Val	Lys
234				_		85		_			90					95	-
236		Leu	Val	Tyr	Arg	Glu	Arg	Lys	Glu	Asn	Val	Phe	Phe	Pro	Leu	Thr	Val
237					100					105					110		
239		Ser	Cys	Ser	Leu	Gly	Cys	Glu	Leu	Pro	Glu	Glu	Glu	Glu	Glu	Gly	Ser
240				115					120					125			
242		Glu		His	Val	Phe	Phe	Asp	Val	Ala	Val	Asn	Gly	Ser	Ala	Phe	Val
243			130					135					140				
245			Phe	Arg	Pro	Lys		Ala	Val	Trp	Val		Gly	Ser	Gln	Glu	
246		145	_				150	_				155		_			160
248		Ser	Lys	Ala	Ala		Phe	Thr	Leu	Lys		Leu	Asn	Ala	Tyr		Arg
249		m1		<b></b>	a1	165	<b>a</b> 1	<b>01</b>	<b>71.</b> -	<b>.</b> .	170		m1	_		175	<b>-1</b>
251		Thr	Arg	Tyr	Glu	ьeu	GIN	GIU	Pne		GIn	Asp	Thr	Cys		GIU	Pne
252		T 0.11	C1	3 0 0	180	т1.	mb ~	mh	<u>ر</u> 1 س	185	Wat	T	C1	0	190	mh	G1
255 256		Leu	GIU	195	His	TTE	Thr	Thr	200	ASI	мес	гàг	GIY	205	GIN	Thr	GTA
258		λνα	Sor		Thr	Sor	Lou	17 a 1		C1 v	т1.	T OU	Mot		Cvc	Dho	т1о
259		ALG	210	TAT	1111	Ser	цец	215	Leu	СТУ	TTE	neu	220	СТУ	Cys	Pile	116
261		Tle		Glv	Va 1	Ala	Va 1		Tle	Phe	Met	Cvs		Ser	Glv	Ara	Gly
262		225		0_1			230	011		1 110	*****	235		JUL	0-1	**** 9	240
264			Leu	Ile	Ile		200					200					210
267	(2)					SEQ I	D NO	): 4	:								
269	(2) INFORMATION FOR SEQ ID NO: 4: (i) SEQUENCE CHARACTERISTICS:																
270		(A) LENGTH: 335 amino acids															
271	(B) TYPE: amino acid																
272			(C)	) STI	RANDI	EDNES	SS: 8	sing	Le								
273			(D)	) TOI	POLO	SY: ]	linea	ar									
275		(ii)	MOLECULE TYPE: peptide														
278		(xi)															
280		Met	Gly	Cys	Leu	Leu	Phe	Leu	Leu	Leu	$\mathtt{Trp}$	Ala	Leu	Leu	Gln	Ala	$\mathtt{Trp}$
281		1		_		5					10					15	_
283		Gly	Ser	Ala	Glu	Val	Pro	Gln	Arg		Phe	Pro	Leu	Arg		Leu	Gln
284		<b>-</b> 1-	<b>G</b>	0	20		•	<b>a</b>	<b>a</b>	25	-1	_	1		30	_	
286		тте	ser		Phe	АТа	Asn	ser		Trp	Thr	Arg	Thr		GТУ	Leu	Ala
287			T	35	a1	T	<b>01</b> -	m b	40	<b>a</b>	Т	<b>a</b>		45	0	•	m1
289 290		тгр	Leu 50	стА	Glu	ьeu	GIN	Thr 55	HIS	ser	тгр	ser		ASP	ser	ASP	Thr
290		V=1		Ser	Leu	Luc	Dro		802	Gln	C1++	ሞሎ∽	60 Bho	G0~	7 c.~	C1 n	C1 n
293		65	n y	∆CT.	пец	пуз	70	115	SET	GIII	ату	75	FIIG	Set	ռոր	GIII	80
200		0.5					, ,					, ,					55



Input Set : N:\Crf3\RULE60\09378261.raw
Output Set: N:\CRF3\01072002\1378261.raw

205		m	C1	mh w	T 011	C1 n	mi a	T10	Dho	3 ma	370.3	m	7 ~~	Cor	Con	Dho	mb
295 296		тър	GIU	Thr	Leu	85	HIS	тте	Pile	AIG	90	тўт	Arg	Ser	261	95	1111
298		Δτα	Δen	Val	T.ve	_	Dhe	Δla	T.ve	Mot		Δrσ	T.011	Ser	TVΥ		T.011
299		nr 9	usb	vui	100	Olu	Tite	niu	цуз	105	пец	nrg	Deu	561	110	110	БСи
301		Glu	Leu	Gln		Ser	Ala	Glv	Cvs		Val	His	Pro	Glv		Ala	Ser
302				115				<b>-</b> 1	120					125			
304		Asn	Asn	Phe	Phe	His	Val	Ala		Gln	Gly	Lys	Asp		Leu	Ser	Phe
305			130					135			•	•	140				
307		Gln	Gly	Thr	Ser	Trp	Glu	Pro	Thr	Gln	Glu	Ala	Pro	Leu	Trp	Val	Asn
308		145					150					155					160
310		Leu	Ala	Ile	Gln	Val	Leu	Asn	Gln	Asp	Lys	Trp	Thr	Arg	Glu	Thr	Val
311						165					170					175	
313		Gln	$\mathtt{Trp}$	Leu		Asn	Gly	Thr	Cys		Gln	Phe	Val	Ser	_	Leu	Leu
314					180					185					190		
317		Glu	Ser	Gly	Lys	Ser	Glu	Leu	_	Lys	Gln	Val	Lys		Lys	Ala	$\mathtt{Trp}$
318				195		_	_		200	_			_	205	_		_
320		Leu		Arg	Gly	Pro	Ser		Gly	Pro	GTA.	Arg		Leu	Leu	Val	Cys
321		** 3 _	210	<b>a</b>	<b>01</b>	<b>5</b> 1	<b></b>	215	<b>.</b>	<b>5</b>	**- 7	<b></b>	220	<b>T</b>		30 - L	•
323			vaı	Ser	GTĀ	Pne	230	Pro	гàг	Pro	vaı	_	vaı	гÃг	Trp	мет	_
324		225	Clu	Gln	Clu	Cln		C117	Thr	Cln.	Dro	235	λan	т1.	Lou	Dro	240
326 327		GIY	GIU	GTII	GIU	245	GIII	СТА	1111	GIII	250	СТА	ASP	116	Leu	255	ASII
329		Δla	Δsn	Glu	Thr		ጥህጕ	T.013	Δτα	Δla		T. <b>2</b> 11	Δsn	Va l	Va 1		Glv
330		niu	пор	OIU	260	115	- 1 -	шси	my	265	1111	пси	пър	vul	270	miu	OI,
332		Glu	Ala	Ala		Leu	Ser	Cvs	Arg		Lvs	His	Ser	Ser		Glu	Glv
333				275	1			-1-	280		-1-			285			1
335		Gln	Asp	Ile	Val	Leu	Tyr	Trp	Gly	Gly	Ser	Tyr	Thr	Ser	Met	Gly	Leu
336			290				-	295	-	-		-	300			-	
338		Ile	Ala	Leu	Ala	Val	Leu	Ala	Cys	Leu	Leu	Phe	Leu	Leu	Ile	Val	Gly
339		305					310					315					320
341		Phe	Thr	Ser	Arg		Lys	Arg	Gln	Thr	Ser	Tyr	Gln	Gly	Val	Leu	
342						325					330					335	
344	(2)	INFO															
346		(i)		JENCI													
347		(A) LENGTH: 336 amino acids (B) TYPE: amino acid															
348				•					1 _								
349				) STI				-	ге								
350 352		/111	•	) TO													
355		, ,	MOLECULE TYPE: peptide SEQUENCE DESCRIPTION: SEQ ID NO: 5:														
357				Tyr								λla	Phe	Leu	Gln	Va 1	Tro
358		1	**** 9	-1-	ncu	5	Cys	LCu	ПСС	Lou	10		1 110	Deu	0111	15	
360			Gln	Ser	Glu	-	Gln	Gln	Lvs	Asn		Thr	Phe	Ara	Cvs		Gln
361		1			20				-1-	25	-1-	<b></b>			30		
363		Thr	Ser	Ser	Phe	Ala	Asn	Ile	Ser	Trp	Ser	Arg	Thr	Asp		Leu	Ile
364				35					40	-		_		45			
366		Leu	Leu	Gly	Asp	Leu	Gln	Thr	His	Arg	Trp	Ser	Asn	Asp	Ser	Ala	Thr
367			50		-			55					60	_			
369		Ile	Ser	Phe	Thr	Lys	Pro	${\tt Trp}$	Ser	Gln	Gly	Lys	Leu	Ser	Asn	Gln	Gln



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PATENT APPLICATION: US/09/378,261

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L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:] L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]